

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/591,109
Source: IFWP
Date Processed by STIC: 09/12/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/591,109

DATE: 09/12/2006

TIME: 11:08:31

Input Set : A:\9052-249.ST25.TXT

Output Set: N:\CRF4\09122006\J591109.raw

3 <110> APPLICANT: Colyer, John
 4 Bhogal, Moninder Singh
 6 <120> TITLE OF INVENTION: METHOD AND PRODUCTS FOR THE SELECTIVE DEGRADATION
 OF PROTEINS
 8 <130> FILE REFERENCE: 9052-249
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/591,109
 C--> 10 <141> CURRENT FILING DATE: 2006-08-31
 10 <150> PRIOR APPLICATION NUMBER: PCT/GB2005/000811
 11 <151> PRIOR FILING DATE: 2005-03-03
 13 <150> PRIOR APPLICATION NUMBER: GB0404731.2
 14 <151> PRIOR FILING DATE: 2004-03-03
 16 <160> NUMBER OF SEQ ID NOS: 12
 18 <170> SOFTWARE: PatentIn version 3.3
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 6
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: misc_feature
 28 <222> LOCATION: (4)..(5)
 29 <223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
 31 <400> SEQUENCE: 1
 W--> 33 Asp Ser Gly Xaa Xaa Ser
 34 1 5
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 26
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: oligonucleotide primer
 45 <400> SEQUENCE: 2
 46 cgggatccat ggataaagtc catacc 26
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 27
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial
 54 <220> FEATURE:
 55 <223> OTHER INFORMATION: oligonucleotide primer
 57 <400> SEQUENCE: 3
 58 cccaagcttt tagagaagca tcaaatg 27
 61 <210> SEQ ID NO: 4
 62 <211> LENGTH: 27
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial

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66 <220> FEATURE:
67 <223> OTHER INFORMATION: oligonucleotide primer
69 <400> SEQUENCE: 4
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73 <210> SEQ ID NO: 5
74 <211> LENGTH: 27
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial
78 <220> FEATURE:
79 <223> OTHER INFORMATION: oligonucleotide primer
81 <400> SEQUENCE: 5
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85 <210> SEQ ID NO: 6
86 <211> LENGTH: 30
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: oligonucleotide primer
93 <400> SEQUENCE: 6
94 cctttgatat tggatcctaa gcttttagag 30
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 45
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial
102 <220> FEATURE:
103 <223> OTHER INFORMATION: oligonucleotide primer
105 <400> SEQUENCE: 7
106 cggtggggga ggcggtgggg gaggcggatc catggataga gtcca 45
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 36
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial
114 <220> FEATURE:
115 <223> OTHER INFORMATION: oligonucleotide primer
117 <400> SEQUENCE: 8
118 catctctaga acctgcaggg aatgcagatc ttcgtg 36
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 45
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: oligonucleotide primer
129 <400> SEQUENCE: 9
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133 <210> SEQ ID NO: 10
134 <211> LENGTH: 24
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:

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139 <223> OTHER INFORMATION: oligonucleotide primer

141 <400> SEQUENCE: 10

142 gggccgctct aaaacccgca ggga

24

145 <210> SEQ ID NO: 11

146 <211> LENGTH: 24

147 <212> TYPE: DNA

148 <213> ORGANISM: Artificial

150 <220> FEATURE:

151 <223> OTHER INFORMATION: oligonucleotide primer

153 <400> SEQUENCE: 11

154 aagcctctag agaagcatca caat

24

157 <210> SEQ ID NO: 12

158 <211> LENGTH: 1349

159 <212> TYPE: PRT

160 <213> ORGANISM: Homo sapiens

162 <400> SEQUENCE: 12

164 Glu Thr Leu Asp Glu Gly Met Gln Ile Pro Ser Thr Gln Phe Asp Ala

165 1 5 10 15

168 Ala His Pro Thr Asn Val Gln Arg Leu Ala Glu Pro Ser Gln Met Leu

169 20 25 30

172 Lys His Ala Val Val Asn Leu Ile Asn Tyr Gln Asp Asp Ala Glu Leu

173 35 40 45

176 Ala Thr Arg Ala Ile Pro Glu Leu Thr Lys Leu Leu Asn Asp Glu Asp

177 50 55 60

180 Gln Val Val Val Asn Lys Ala Ala Val Met Val His Gln Leu Ser Lys

181 65 70 75 80

184 Lys Glu Ala Ser Arg His Ala Ile Met Arg Ser Pro Gln Met Val Ser

185 85 90 95

188 Ala Ile Val Arg Thr Met Gln Asn Thr Asn Asp Val Glu Thr Ala Arg

189 100 105 110

192 Cys Thr Ala Gly Thr Leu His Asn Leu Ser His His Arg Glu Gly Leu

193 115 120 125

196 Leu Ala Ile Phe Lys Ser Gly Gly Ile Pro Ala Leu Val Lys Met Leu

197 130 135 140

200 Gly Ser Pro Val Asp Ser Val Leu Phe Tyr Ala Ile Thr Thr Leu His

201 145 150 155 160

204 Asn Leu Leu Leu His Gln Glu Gly Ala Lys Met Ala Val Arg Leu Ala

205 165 170 175

208 Gly Gly Leu Gln Lys Met Val Ala Leu Leu Asn Lys Thr Asn Val Lys

209 180 185 190

212 Phe Leu Ala Ile Thr Thr Asp Cys Leu Gln Ile Leu Ala Tyr Gly Asn

213 195 200 205

216 Gln Glu Ser Lys Leu Ile Ile Leu Ala Ser Gly Gly Pro Gln Ala Leu

217 210 215 220

220 Val Asn Ile Met Arg Thr Tyr Thr Tyr Glu Lys Leu Leu Trp Thr Thr

221 225 230 235 240

224 Ser Arg Val Leu Lys Val Leu Ser Val Cys Ser Ser Asn Lys Pro Ala

225 245 250 255

228 Ile Val Glu Ala Gly Gly Met Gln Ala Leu Gly Leu His Leu Thr Asp

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229          260          265          270
232 Pro Ser Gln Arg Leu Val Gln Asn Cys Leu Trp Thr Leu Arg Asn Leu
233          275          280          285
236 Ser Asp Ala Ala Thr Lys Gln Glu Gly Met Glu Gly Leu Leu Gly Thr
237          290          295          300
240 Leu Val Gln Leu Leu Gly Ser Asp Asp Ile Asn Val Val Thr Cys Ala
241 305          310          315          320
244 Ala Gly Ile Leu Ser Asn Leu Thr Cys Asn Asn Tyr Lys Asn Lys Met
245          325          330          335
248 Met Val Cys Gln Val Gly Gly Ile Glu Ala Leu Val Arg Thr Val Leu
249          340          345          350
252 Arg Ala Gly Asp Arg Glu Asp Ile Thr Glu Pro Ala Ile Cys Ala Leu
253          355          360          365
256 Arg His Leu Thr Ser Arg His Gln Glu Ala Glu Met Ala Gln Asn Ala
257          370          375          380
260 Val Arg Leu His Tyr Gly Leu Pro Val Val Val Lys Leu Leu His Pro
261 385          390          395          400
264 Pro Ser His Trp Pro Leu Ile Lys Ala Thr Val Gly Leu Ile Arg Asn
265          405          410          415
268 Leu Ala Leu Cys Pro Ala Asn His Ala Pro Leu Arg Glu Gln Gly Ala
269          420          425          430
272 Ile Pro Arg Leu Val Gln Leu Leu Val Arg Ala His Gln Asp Thr Gln
273          435          440          445
276 Arg Arg Thr Ser Met Gly Gly Thr Gln Gln Gln Phe Val Glu Gly Val
277          450          455          460
280 Arg Met Glu Glu Ile Val Glu Gly Cys Thr Gly Ala Leu His Ile Leu
281 465          470          475          480
284 Ala Arg Asp Val His Asn Arg Ile Val Ile Arg Gly Leu Asn Thr Ile
285          485          490          495
288 Pro Leu Phe Val Gln Leu Leu Tyr Ser Pro Ile Glu Asn Ile Gln Arg
289          500          505          510
292 Val Ala Ala Gly Val Leu Cys Glu Leu Ala Gln Asp Lys Glu Ala Ala
293          515          520          525
296 Glu Ala Ile Glu Ala Glu Gly Ala Thr Ala Pro Leu Thr Glu Leu Leu
297          530          535          540
300 His Ser Arg Asn Glu Gly Val Ala Thr Tyr Ala Ala Ala Val Leu Phe
301 545          550          555          560
304 Arg Met Ser Glu Asp Lys Pro Gln Asp Tyr Lys Lys Arg Leu Ser Val
305          565          570          575
308 Glu Leu Thr Ser Ser Leu Phe Arg Thr Glu Pro Met Ala Trp Asn Glu
309          580          585          590
312 Thr Ala Asp Leu Gly Leu Asp Ile Gly Ala Gln Gly Glu Ala Leu Gly
313          595          600          605
316 Tyr Arg Gln Asp Asp Pro Ser Tyr Arg Ser Phe His Ser Gly Gly Tyr
317          610          615          620
320 Gly Gln Asp Ala Leu Gly Met Asp Pro Met Met Glu His Glu Met Gly
321 625          630          635          640
324 Gly His His Pro Gly Ala Asp Tyr Pro Val Asp Gly Leu Pro Asp Leu
325          645          650          655

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328 Gly His Ala Gln Asp Leu Met Asp Gly Leu Pro Pro Gly Asp Ser Asn
329           660           665           670
332 Gln Leu Ala Trp Phe Asp Thr Asp Leu Gly Ser Asn Met Asp Pro Ala
333           675           680           685
336 Glu Ala Val Leu Gln Glu Lys Ala Leu Lys Phe Met Asn Ser Ser Glu
337           690           695           700
340 Arg Glu Asp Cys Asn Asn Gly Glu Pro Pro Arg Lys Ile Ile Pro Glu
341 705           710           715           720
344 Lys Asn Ser Leu Arg Gln Thr Tyr Asn Ser Cys Ala Arg Leu Cys Ile
345           725           730           735
348 Asn Gln Glu Thr Val Cys Leu Thr Ser Thr Ala Met Lys Thr Glu Asn
349           740           745           750
352 Cys Val Ala Lys Ala Lys Leu Ala Asn Gly Thr Ser Ser Met Ile Val
353           755           760           765
356 Pro Lys Gln Arg Lys Leu Ser Ala Ser Tyr Glu Lys Glu Lys Glu Leu
357           770           775           780
360 Cys Val Lys Tyr Phe Glu Gln Trp Ser Glu Ser Asp Gln Val Glu Phe
361 785           790           795           800
364 Val Glu His Leu Ile Ser Gln Met Cys His Tyr Gln His Gly His Ile
365           805           810           815
368 Asn Ser Tyr Leu Lys Pro Met Leu Gln Arg Asp Phe Ile Thr Ala Leu
369           820           825           830
372 Pro Ala Arg Gly Leu Asp His Ile Ala Glu Asn Ile Leu Ser Tyr Leu
373           835           840           845
376 Asp Ala Lys Ser Leu Cys Ala Ala Glu Leu Val Cys Lys Glu Trp Tyr
377           850           855           860
380 Arg Val Thr Ser Asp Gly Met Leu Trp Lys Lys Leu Ile Glu Arg Met
381 865           870           875           880
384 Val Arg Thr Asp Ser Leu Trp Arg Gly Leu Ala Glu Arg Arg Gly Trp
385           885           890           895
388 Gly Gln Tyr Leu Phe Lys Asn Lys Pro Pro Asp Glu Asn Ala Pro Pro
389           900           905           910
392 Asn Ser Phe Tyr Arg Ala Leu Tyr Pro Lys Ile Ile Gln Asp Ile Glu
393           915           920           925
396 Thr Ile Glu Ser Asn Trp Arg Cys Gly Arg His Ser Leu Gln Arg Ile
397           930           935           940
400 His Cys Arg Ser Glu Thr Ser Lys Gly Val Tyr Cys Leu Gln Tyr Asp
401 945           950           955           960
404 Asp Gln Lys Ile Val Ser Gly Leu Arg Asp Asn Thr Ile Lys Ile Trp
405           965           970           975
408 Asp Lys Ser Thr Leu Glu Cys Lys Arg Ile Leu Thr Gly His Thr Gly
409           980           985           990
412 Ser Val Leu Cys Leu Gln Tyr Asp Glu Arg Val Ile Ile Thr Gly Ser
413           995           1000           1005
416 Ser Asp Ser Thr Val Arg Val Trp Asp Val Asn Ala Gly Glu Met
417           1010           1015           1020
420 Leu Asn Thr Leu Ile His His Cys Glu Ala Val Leu His Leu Arg
421           1025           1030           1035
424 Phe Asn Asn Gly Met Met Val Thr Cys Ser Lys Asp Arg Ser Ile

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 4,5

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0